



Print

1. $\frac{1}{2} \times \frac{1}{2} = \frac{1}{4}$ (Probability of getting two heads)

REF ID	REF DATE	LANGUAGE	PAGES	MAIN ID
DE 00000700 H	February 13, 2000		000	012N0010-14
AL 2000090000 AL	February 14, 2000	H	001	012N0010-14
AL 00000000 A	March 8, 2000		001	012N0010-14
DE 11000000 AL	June 13, 2000	H	000	012N0010-14
DE 200000000000 AL	May 20, 2000		000	012Q0000-00
DE 12000000 AL	August 14, 2000	H	000	012N0010-14
DE 200000000000 W	July 28, 2000		029	012N0010-09
DE 11000000 H	September 4, 2000	H	000	012N0010-14

DATE	TIME	STARTED	AM	AL	AN	AT	AV	BA	BE	BF	BT	CA	CH	CI	CL	CO	CR	CS	CU	CV	DA	DE	DF	DG	DI	DR	DS	DT	DU	EA	EB	EC	ED	EE	EF	EG	EH	EI	EJ	EK	EL	EM	EN	EO	EP	EQ	ER	ES	ET	EU	EV	EW	EX	EY	EZ	FA	FB	FC	FD	FE	FF	FG	FH	FI	FJ	FK	FL	FM	FN	FO	FP	FQ	FR	FS	FT	FU	FV	FW	FX	FY	FZ	GA	GB	GC	GD	GE	GF	GG	GH	GI	GJ	GK	GL	GM	GN	GO	GP	GQ	GR	GS	GT	GU	GV	GW	GX	GY	GZ	HA	HB	HC	HD	HE	HF	HG	HH	HI	HJ	HK	HL	HM	HN	HO	HP	HQ	HR	HS	HT	HU	HV	HW	HX	HY	HZ	IA	IB	IC	ID	IE	IF	IG	IH	II	IJ	IK	IL	IM	IN	IO	IP	IQ	IR	IS	IT	IU	IV	IW	IX	IY	IZ	JA	JB	JC	JD	JE	JF	JG	JH	JI	IJ	JK	JL	JM	JN	JO	JP	JQ	JR	JS	JT	JU	JV	JW	JX	JY	JZ	KA	KB	KC	KD	KE	KF	KG	KH	KI	KJ	KK	KL	KM	KN	KO	KP	KQ	KR	KS	KT	KU	KV	KW	KX	KY	KZ	LA	LB	LC	LD	LE	LF	LG	LH	LI	LJ	LK	LM	LN	LO	LP	LQ	LR	LS	LT	LU	LV	LW	LX	LY	LZ	MA	MB	MC	MD	ME	MF	MG	MH	MI	MJ	MK	ML	MM	MN	MO	MP	MQ	MR	MS	MT	MU	MV	MW	MX	MY	MZ	NA	NB	NC	ND	NE	NF	NG	NH	NI	NJ	NK	NL	NM	NN	NO	NP	NQ	NR	NS	NT	NU	NV	NW	NX	NY	NZ	OA	OB	OC	OD	OE	OF	OG	OH	OI	OJ	OK	OL	OM	ON	OO	OP	OQ	OR	OS	OT	OU	OV	OW	OX	OY	OZ	PA	PB	PC	PD	PE	PF	PG	PH	PI	PJ	PK	PL	PM	PN	PO	PP	PQ	PR	PS	PT	PU	PV	PW	PX	PY	PZ	QA	QB	QC	QD	QE	QF	QG	QH	QI	QJ	QK	QL	QM	QN	QO	QP	QQ	QR	QS	QT	QU	QV	QW	QX	QY	QZ	RA	RB	RC	RD	RE	RF	RG	RH	RI	RJ	RK	RL	RM	RN	RO	RP	RQ	RR	RS	RT	RU	RV	RW	RX	RY	RZ	SA	SB	SC	SD	SE	SF	SG	SH	SI	SJ	SK	SL	SM	SN	SO	SP	SQ	SR	SS	ST	SU	SV	SW	SX	SY	SZ	TA	TB	TC	TD	TE	TF	TG	TH	TI	TJ	TK	TL	TM	TN	TO	TP	TQ	TR	TS	TT	TU	TV	TW	TX	TY	TZ	UA	UB	UC	UD	UE	UF	UG	UH	UI	UJ	UK	UL	UM	UN	UO	UP	UQ	UR	US	UT	UU	UV	UW	UX	UY	UZ	VA	VB	VC	VD	VE	VF	VG	VH	VI	VJ	VK	VL	VM	VN	VO	VP	VQ	VR	VS	VT	VU	VV	VW	VX	VY	VZ	WA	WB	WC	WD	WE	WF	WG	WH	WI	WJ	WK	WL	WM	WN	WO	WP	WQ	WR	WS	WT	WU	WV	WW	WX	WY	WZ	XA	XB	XC	XD	XE	XF	XG	XH	XI	XJ	XK	XL	XM	XN	XO	XP	XQ	XR	XS	XT	XU	XV	XW	XX	XY	XZ	YA	YB	YC	YD	YE	YF	YG	YH	YI	YJ	YK	YL	YM	YN	YO	YP	YQ	YR	YS	YT	YU	YV	YW	YX	YY	YZ	ZA	ZB	ZC	ZD	ZE	ZF	ZG	ZH	ZI	ZJ	ZK	ZL	ZM	ZN	ZO	ZP	ZQ	ZR	ZS	ZT	ZU	ZV	ZW	ZX	ZY	ZZ
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1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100

Summary:

1. providing an expression construct (a) containing a polypeptide or subunit of a protein complex, each being fused to at least 2 different affinity tags, one of which consists of one or more IgG binding domains of S₁A;

2. maintaining the expression or, when it is desirable, expression of the gene of 1) in a suitable host cell in form of a fusion protein with the affinity tags, and 3) allowing formation of a complex between the one or more subunits and possibly other components capable of complexing with the one or more subunits; and

3. detecting and/or purifying the complex by a combination of at least 2 different affinity purification steps each comprising binding the one or more subunits via one affinity tag to a support material capable of selectively binding one of the affinity tags and separating the complex from the support material after unbound substances have been removed;

2. fusion proteins comprising at least one polypeptide or subunit of a protein complex fused to at least 2 different affinity tags, where one of the affinity tags consists of at least one IgG binding domain of S₁A;

3. nucleic acid coding for a fusion protein of 2);

4. a vector comprising a nucleic acid as in 3) under the control of sequences facilitating the expression of a fusion protein as in 2);

5. a vector comprising heterologous nucleic acid sequences in form of one or more cassettes each comprising at least 2 different affinity tags, one consisting of one or more IgG binding domains of Staphylococcus aureus protein A (S₁APA), and at least one PN linker for the insertion of further nucleic acids;

6. a vector comprising heterologous nucleic acid sequences in form of 2 or more cassettes each comprising at least one of different affinity tags, one consisting of one or more IgG binding domains of S₁APA, and at least one PN linker for the insertion of further nucleic acids;

7. a cell containing a nucleic acid of 3) or a vector of 4); and

8. a reagent kit comprising a nucleic acid of 3) or a vector of 4), 5) or 6) for the expression of a fusion protein of 2) and support materials each capable of specifically binding one of the affinity tags.

USE: The methods can be used for the detection and/or purification of substances capable of complexing with the fusion protein claimed. They can also be used for the detection and/or purification of cells and/or cell organelles expressing the fusion protein on their surface claimed. They can be used for studying the structure, activities or interactions with proteins or nucleic acids. The methods not only facilitate efficient purification of proteins of interest but also allows fishing for and detecting components present in complexes with which the polypeptides or subunits are associated or complexed either directly or indirectly, e.g. molecules such as linker mediators. This would allow selective fishing for certain substances which may be potential drugs, even from complex mixtures.

ABSTRACT FOR NON-PROFESSOR ABSTRACT EQUIVALENT ABSTRACT:

NOVELTY: A method for detecting and purifying substances uses polypeptides or subunits fused to at least 2 different affinity tags, at least one of which is an IgG binding domain of Staphylococcus aureus protein A (S₁APA).

DETAILED DESCRIPTION: A method for detecting and purifying substances from proteins or cell organelles complexed together and/or with other components such as linker mediators and other components.

a) providing an expression environment containing one or more heterologous nucleic acids encoding polypeptides and/or subunits of a protein complex, each being fused to at least one of different affinity tags, one of which consists of one or more IgG binding domains of SPA;

b) maintaining the expression environment to express the polypeptides or subunits in a native form as fusion proteins with the affinity tags; and

c) detecting and/or purifying the polypeptides or subunits by a combination of at least 2 affinity purification steps each comprising binding the polypeptides or subunits via one affinity tag to a support material capable of selectively binding one of the affinity tags and separating the polypeptides or subunits from the support material after unbound substances have been removed.

INDEPENDENT CLAIMS are also included for the following:

1. a method for detecting and/or purifying a) a molecule and b) protein complexes comprising:

a) providing an expression environment containing one or more heterologous nucleic acids encoding at least 2 subunits of a protein complex, each being fused to at least one of different affinity tags, one of which consists of one or more IgG binding domains of SPA;

b) maintaining the expression environment to facilitate expression of the one or more subunits in a native form as fusion proteins with the affinity tags, and to allow formation of a complex between the one or more subunits and possibly other components capable of complexing with the one or more subunits; and

c) detecting and/or purifying the complex by a combination of at least 2 different affinity purification steps each comprising binding the one or more subunits via one affinity tag to a support material capable of selectively binding one of the affinity tags and separating the complex from the support material after unbound substances have been removed;

2. fusion protein comprising at least one polypeptide or subunit of a protein complex fused to at least 2 different affinity tags, where one of the affinity tags consists of at least one IgG binding domain of SPA;

3. nucleic acid coding for a fusion protein of 1.;

4. a vector comprising a nucleic acid as in 3 under the control of sequences facilitating the expression of a fusion protein as in 2.;

5. a vector comprising heterologous nucleic acid sequences in form of one or more cassettes each comprising at least 2 different affinity tags, one consisting of one or more IgG binding domains of Staphylococcus aureus protein A (SAPA), and at least one RN linker for the insertion of further nucleic acids;

6. a vector comprising heterologous nucleic acid sequences in form of 1 or more cassettes each comprising at least one of different affinity tags, one consisting of one or more IgG binding domains of SAPA, and at least one RN linker for the insertion of further nucleic acids;

7. a cell containing a nucleic acid of 3 or a vector of 4, 5 and

8. a reagent kit comprising a nucleic acid of 3 or a vector of 4, 5 or 6 for the expression of a fusion protein of 2 and support materials each capable of specifically binding one of the affinity tags.

USP: The methods can be used for the detection and purification of substances capable of complexing with the fusion proteins claimed. They can also be used for the detection and purification of cells and/or cells engineered expressing the fusion proteins of interest. Substances claimed. They can be used for studying the structure, activities, interactions and with proteins of various nature. The method is not only

facilitating efficient purification of proteins of interest but also allowing detection and detection components present and compared with which the polypeptides or subunits are analyzed or improved either directly or indirectly, e.g., by means such as linker-mediated ligation and direct recombination, for certain substances which may be potential drugs, even from complex mixtures.

NOVELTY A method for detecting and/or purifying substances (e.g., polypeptides or subunits) fused to at least 2 different affinity tags, at least one of which is an IgG binding domain of staphylococcal protein A (SPA).

DETAILED DESCRIPTION A method of detecting and/or purifying substances selected from proteins, DNA molecules, complexed proteins and molecules, subunits, cell components, cell organelles and cells, comprises:

- a. providing an expression environment containing one or more heterologous nucleic acids encoding polypeptides and/or subunits of a biomolecule complex, the polypeptides or subunits being fused to at least 2 different affinity tags, one of which consists of one or more IgG binding domains of SPA;
- b. maintaining the expression environment to express the polypeptides or subunits in a native form as fusion proteins with the affinity tags; and
- c. detecting and/or purifying the polypeptide or subunits by a combination of at least 2 affinity purification steps, each comprising binding the polypeptides or subunits via one affinity tag to a support material capable of selectively binding one of the affinity tags and separating the polypeptides or subunits from the support material after unbound substances have been removed.

INDEPENDENT CLAIMS are also included for the following:

- 1. a method for detecting and/or purifying biomolecule and/or protein complexes comprising:
 - a. providing an expression environment containing one or more heterologous nucleic acids encoding at least 2 subunits of a biomolecule complex, each being fused to at least one of different affinity tags, one of which consists of one or more IgG binding domains of SPA;
 - b. maintaining the expression environment to facilitate expression of the one or more subunits in a native form as fusion proteins with the affinity tags, and to allow formation of a complex between the one or more subunits and possibly other components capable of complexing with the one or more subunits; and
 - c. detecting and/or purifying the complex by a combination of at least 2 different affinity purification steps each comprising binding the one or more subunits via one affinity tag to a support material capable of selectively binding one of the affinity tags and separating the complex from the support material after unbound substances have been removed;
- 2. fusion protein comprising at least one polypeptide or subunit of a protein complex fused to at least 2 different affinity tags, where one of the affinity tags consists of at least one IgG binding domain of SPA;
- 3. nucleic acid coding for a fusion protein of (2);
- 4. a vector comprising a nucleic acid as in (3) under the control of sequences facilitating the expression of a fusion protein as in (2);
- 5. a vector comprising heterologous nucleic acid sequences in form of one or more cassettes each comprising at least 2 different affinity tags, one consisting of one or more IgG binding domains of staphylococcal protein A (SPA), and at least one linker for the insertion of heterologous nucleic acids;
- 6. a vector comprising heterologous nucleic acid sequences in form of one or more cassettes each comprising at least one of different affinity tags, one consisting of

¹¹ A well-known theorem of Nielsen and Schreier states that if H is a section of G , and

USE. The resin or can be used for the detection and/or purification of substances capable of complexing with the fusion protein claimed. They can also be used for the detection and/or purification of cells and/or cell organelles expressing the fusion protein on their surface claimed. They can be used for studying the structure, activities or interactions with proteins or nucleic acids. The methods not only facilitate efficient purification of proteins of interest but also allows fishing for and detecting components present in complexes with which the polypeptides or subunits are associated or complexed either directly or indirectly, e.g. molecules such as linker mediators. This would allow selective fishing, for certain substances which may be potential drugs, even from complex mixtures.

DESIGNER: **DAVID COOPER**

[illegible]